

10/560760

43

IAP2007-00000000 14 DEC 2005

## SEQUENCE LISTING

&lt;110&gt; Evologic S.A.

Maliere Technologies Société Civile

Rhodia Chimie

Marliere, Phillipe

&lt;120&gt; Cloning of gluconate dehydratase gcnD gene

&lt;130&gt; G 3111 EP

&lt;160&gt; 33

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1812

&lt;212&gt; DNA

&lt;213&gt; Agrobacterium tumefaciens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1809)

&lt;223&gt;

&lt;400&gt; 1

atg acg aca tct gat aat ctt cct gca act cag ggc aag ctc cgt tcg	48
Met Thr Thr Ser Asp Asn Leu Pro Ala Thr Gln Gly Lys Leu Arg Ser	
1 5 10 15	
cgc gcc tgg ttc gac aac cca gcc aat gcg gac atg acc gcg ctt tat	96
Arg Ala Trp Phe Asp Asn Pro Ala Asn Ala Asp Met Thr Ala Leu Tyr	
20 25 30	
ctc gag cgt tac atg aac ttc ggt ctc agc cag gcc gag ctt cag tcc	144
Leu Glu Arg Tyr Met Asn Phe Gly Leu Ser Gln Ala Glu Leu Gln Ser	
35 40 45	

gac cgc ccg att atc ggt att gcg cag acc ggt tcc gac ctt tcg ccc Asp Arg Pro Ile Ile Gly Ile Ala Gln Thr Gly Ser Asp Leu Ser Pro 50 55 60	192
tgc aac cgt cat cat ctg gaa ctc gcc aac cgt ctg cgt gaa ggc att Cys Asn Arg His His Leu Glu Leu Ala Asn Arg Leu Arg Glu Gly Ile 65 70 75 80	240
cgt gaa gcc ggc ggc atc gcc atc gaa ttc ccg gtg cat ccg atc cag Arg Glu Ala Gly Gly Ile Ala Ile Glu Phe Pro Val His Pro Ile Gln 85 90 95	288
gaa acc ggt aag cgt ccg aca gcg ggc ctt gat cgc aac ctg gct tac Glu Thr Gly Lys Arg Pro Thr Ala Gly Leu Asp Arg Asn Leu Ala Tyr 100 105 110	336
ctc ggc ctc gtg gaa gtg ctt tat ggc tat ccg ctc gac ggc gtt gtt Leu Gly Leu Val Glu Val Leu Tyr Gly Tyr Pro Leu Asp Gly Val Val 115 120 125	384
ctg acc atc ggc tgc gac aag acc acg cct gcc tgt ctt atg gcg gcg Leu Thr Ile Gly Cys Asp Lys Thr Thr Pro Ala Cys Leu Met Ala Ala 130 135 140	432
gcc acc gtc aac att ccg gcc atc gcc ctt tcc gtc ggt ccc atg ctg Ala Thr Val Asn Ile Pro Ala Ile Ala Leu Ser Val Gly Pro Met Leu 145 150 155 160	480
aac ggc tgg ttc cgc ggt gag cgc acc ggt tcc ggc acc atc gtc tgg Asn Gly Trp Phe Arg Gly Glu Arg Thr Gly Ser Gly Thr Ile Val Trp 165 170 175	528
aag gcc cgc gaa ctg ctg gcg aag ggc gag atc gat tac cag ggc ttc Lys Ala Arg Glu Leu Leu Ala Lys Gly Glu Ile Asp Tyr Gln Gly Phe 180 185 190	576
gtc aag ctc gtt gcc tcg tct gcc ccg tcc acc ggc tat tgc aac acc Val Lys Leu Val Ala Ser Ser Ala Pro Ser Thr Gly Tyr Cys Asn Thr 195 200 205	624
atg ggc acg gca aca acc atg aac tcg ctc gcc gaa gcg ctc ggc atg Met Gly Thr Ala Thr Thr Met Asn Ser Leu Ala Glu Ala Leu Gly Met 210 215 220	672
cag ctt ccc ggc tcc gcc gcc att ccg gcg cct tac cgt gac cgt cag Gln Leu Pro Gly Ser Ala Ala Ile Pro Ala Pro Tyr Arg Asp Arg Gln 225 230 235 240	720
gaa gtc tct tac ctc acc ggc ctg cgc atc gtc gac atg gtc agg gaa Glu Val Ser Tyr Leu Thr Gly Leu Arg Ile Val Asp Met Val Arg Glu 245 250 255	768
gac ctg aaa cca tca gac atc atg acc aag gat gcc ttc atc aac gcc Asp Leu Lys Pro Ser Asp Ile Met Thr Lys Asp Ala Phe Ile Asn Ala 260 265 270	816
atc cgc gtt aat tcg gcg atc ggc ggt tcc acc aac gcg ccg atc cat Ile Arg Val Asn Ser Ala Ile Gly Gly Ser Thr Asn Ala Pro Ile His 275 280 285	864

cta aac ggc ctt gcc cgc cat gtc ggc gtc gag ctg acg gtg gat gac Leu Asn Gly Leu Ala Arg His Val Gly Val Glu Leu Thr Val Asp Asp 290 295 300	912
tgg cag acc tat ggc gaa gac gtg ccg ctg ctc gtc aac ctg cag ccg Trp Gln Thr Tyr Gly Glu Asp Val Pro Leu Leu Val Asn Leu Gln Pro 305 310 315 320	960
gca ggc gaa tat ctc ggc gag gac tat tac cat gcc ggc ggc gtt ccc Ala Gly Glu Tyr Leu Gly Glu Asp Tyr Tyr His Ala Gly Gly Val Pro 325 330 335	1008
gct gtc gtc aat cag ctg atg acc caa ggg ctg atc atg gaa gac gcc Ala Val Val Asn Gln Leu Met Thr Gln Gly Leu Ile Met Glu Asp Ala 340 345 350	1056
atg acc gtc aac ggc aag acc atc ggc gac aat tgc cgt ggc gcg atc Met Thr Val Asn Gly Lys Thr Ile Gly Asp Asn Cys Arg Gly Ala Ile 355 360 365	1104
atc gaa gac gag aag gtc atc cgc ccc tat gag cag ccg ctc aag gag Ile Glu Asp Glu Lys Val Ile Arg Pro Tyr Glu Gln Pro Leu Lys Glu 370 375 380	1152
cgt gcc ggc ttc cgc gtt ctg cgc ggc aat ctg ttc tcc tcg gcc atc Arg Ala Gly Phe Arg Val Leu Arg Gly Asn Leu Phe Ser Ser Ala Ile 385 390 395 400	1200
atg aag aca agc gtg att tcg gaa gaa ttc cgc ggt cgt tac ctc tcc Met Lys Thr Ser Val Ile Ser Glu Glu Phe Arg Gly Arg Tyr Leu Ser 405 410 415	1248
aac cct gat gat ccg gaa gcc ttc gaa ggc cgc gcc gtg gtg ttc gat Asn Pro Asp Asp Pro Glu Ala Phe Glu Gly Arg Ala Val Val Phe Asp 420 425 430	1296
ggt ccg gag gat tac cat cat cgc atc gac gat ccg tcg ctt ggc atc Gly Pro Glu Asp Tyr His His Arg Ile Asp Asp Pro Ser Leu Gly Ile 435 440 445	1344
gac gcc aac acc gtc ctg ttc atg cgc ggc gcc ggt ccg atc ggt tac Asp Ala Asn Thr Val Leu Phe Met Arg Gly Ala Gly Pro Ile Gly Tyr 450 455 460	1392
ccg ggc gca gcg gaa gtg gtg aac atg cgc gcg ccg gat tac ctt ctg Pro Gly Ala Ala Glu Val Val Asn Met Arg Ala Pro Asp Tyr Leu Leu 465 470 475 480	1440
aag caa ggc gtc agt tcg ctg ccc tgc atc ggc gat ggc cgc cag tcc Lys Gln Gly Val Ser Ser Leu Pro Cys Ile Gly Asp Gly Arg Gln Ser 485 490 495	1488
ggc acg tcg ggc agc cca tcc atc ctc aat gcc tcg ccg gaa gcg gcg Gly Thr Ser Gly Ser Pro Ser Ile Leu Asn Ala Ser Pro Glu Ala Ala 500 505 510	1536
gcc gcc ggc ggt ctg tct att ctg cag acg ggt gac cgc gtc cgc atc Ala Gly Gly Gly Leu Ser Ile Leu Gln Thr Gly Asp Arg Val Arg Ile 515 520 525	1584

gat gtg ggc cgc ggc aag gcc gat atc ctg ata tca ggt gaa gag ctc 1632  
 Asp Val Gly Arg Gly Lys Ala Asp Ile Leu Ile Ser Gly Glu Glu Leu  
 530 535 540

gcc aag cgt tac gag gcg ctg gca gct cag ggc ggt tat aag ttc ccc 1680  
 Ala Lys Arg Tyr Glu Ala Leu Ala Ala Gln Gly Gly Tyr Lys Phe Pro  
 545 550 555 560

gac cac cag acg ccg tgg cag gaa atc cag cgc ggt atc gtc agc cag 1728  
 Asp His Gln Thr Pro Trp Gln Glu Ile Gln Arg Gly Ile Val Ser Gln  
 565 570 575

atg gaa acc ggc gcg gtt ctg gaa ccg gcc gta aag tat cag cgc atc 1776  
 Met Glu Thr Gly Ala Val Leu Glu Pro Ala Val Lys Tyr Gln Arg Ile  
 580 585 590

gcc cag acc aag ggc ctg ccg cgc gat aac cac tga 1812  
 Ala Gln Thr Lys Gly Leu Pro Arg Asp Asn His  
 595 600

<210> 2

<211> 603

<212> PRT

<213> Agrobacterium tumefaciens

<400> 2

Met Thr Thr Ser Asp Asn Leu Pro Ala Thr Gln Gly Lys Leu Arg Ser  
 1 5 10 15

Arg Ala Trp Phe Asp Asn Pro Ala Asn Ala Asp Met Thr Ala Leu Tyr  
 20 25 30

Leu Glu Arg Tyr Met Asn Phe Gly Leu Ser Gln Ala Glu Leu Gln Ser  
 35 40 45

Asp Arg Pro Ile Ile Gly Ile Ala Gln Thr Gly Ser Asp Leu Ser Pro  
 50 55 60

Cys Asn Arg His His Leu Glu Leu Ala Asn Arg Leu Arg Glu Gly Ile  
 65 70 75 80

Arg Glu Ala Gly Gly Ile Ala Ile Glu Phe Pro Val His Pro Ile Gln  
 85 90 95

Glu Thr Gly Lys Arg Pro Thr Ala Gly Leu Asp Arg Asn Leu Ala Tyr  
 100 105 110

Leu Gly Leu Val Glu Val Leu Tyr Gly Tyr Pro Leu Asp Gly Val Val  
 115 120 125

Leu Thr Ile Gly Cys Asp Lys Thr Thr Pro Ala Cys Leu Met Ala Ala  
 130 135 140

Ala Thr Val Asn Ile Pro Ala Ile Ala Leu Ser Val Gly Pro Met Leu  
 145 150 155 160

Asn Gly Trp Phe Arg Gly Glu Arg Thr Gly Ser Gly Thr Ile Val Trp  
 165 170 175

Lys Ala Arg Glu Leu Leu Ala Lys Gly Glu Ile Asp Tyr Gln Gly Phe  
 180 185 190

Val Lys Leu Val Ala Ser Ser Ala Pro Ser Thr Gly Tyr Cys Asn Thr  
 195 200 205

Met Gly Thr Ala Thr Thr Met Asn Ser Leu Ala Glu Ala Leu Gly Met  
 210 215 220

Gln Leu Pro Gly Ser Ala Ala Ile Pro Ala Pro Tyr Arg Asp Arg Gln  
 225 230 235 240

Glu Val Ser Tyr Leu Thr Gly Leu Arg Ile Val Asp Met Val Arg Glu  
 245 250 255

Asp Leu Lys Pro Ser Asp Ile Met Thr Lys Asp Ala Phe Ile Asn Ala  
 260 265 270

Ile Arg Val Asn Ser Ala Ile Gly Gly Ser Thr Asn Ala Pro Ile His  
 275 280 285

Leu Asn Gly Leu Ala Arg His Val Gly Val Glu Leu Thr Val Asp Asp  
 290 295 300

Trp Gln Thr Tyr Gly Glu Asp Val Pro Leu Leu Val Asn Leu Gln Pro  
 305 310 315 320

Ala Gly Glu Tyr Leu Gly Glu Asp Tyr Tyr His Ala Gly Gly Val Pro  
 325 330 335

Ala Val Val Asn Gln Leu Met Thr Gln Gly Leu Ile Met Glu Asp Ala  
 340 345 350

Met Thr Val Asn Gly Lys Thr Ile Gly Asp Asn Cys Arg Gly Ala Ile  
 355 360 365

Ile Glu Asp Glu Lys Val Ile Arg Pro Tyr Glu Gln Pro Leu Lys Glu  
 370 375 380

Arg Ala Gly Phe Arg Val Leu Arg Gly Asn Leu Phe Ser Ser Ala Ile  
 385 390 395 400

Met Lys Thr Ser Val Ile Ser Glu Glu Phe Arg Gly Arg Tyr Leu Ser  
 405 410 415

Asn Pro Asp Asp Pro Glu Ala Phe Glu Gly Arg Ala Val Val Phe Asp  
 420 425 430

Gly Pro Glu Asp Tyr His His Arg Ile Asp Asp Pro Ser Leu Gly Ile  
 435 440 445

Asp Ala Asn Thr Val Leu Phe Met Arg Gly Ala Gly Pro Ile Gly Tyr  
 450 455 460

Pro Gly Ala Ala Glu Val Val Asn Met Arg Ala Pro Asp Tyr Leu Leu  
 465 470 475 480

Lys Gln Gly Val Ser Ser Leu Pro Cys Ile Gly Asp Gly Arg Gln Ser  
 485 490 495

Gly Thr Ser Gly Ser Pro Ser Ile Leu Asn Ala Ser Pro Glu Ala Ala  
 500 505 510

Ala Gly Gly Gly Leu Ser Ile Leu Gln Thr Gly Asp Arg Val Arg Ile  
 515 520 525

Asp Val Gly Arg Gly Lys Ala Asp Ile Leu Ile Ser Gly Glu Glu Leu  
 530 535 540

Ala Lys Arg Tyr Glu Ala Leu Ala Ala Gln Gly Gly Tyr Lys Phe Pro  
 545 550 555 560

Asp His Gln Thr Pro Trp Gln Glu Ile Gln Arg Gly Ile Val Ser Gln  
 565 570 575

Met Glu Thr Gly Ala Val Leu Glu Pro Ala Val Lys Tyr Gln Arg Ile  
 580 585 590

Ala Gln Thr Lys Gly Leu Pro Arg Asp Asn His  
 595 600

<210> 3

<211> 1272

<212> DNA

<213> Agrobacterium tumefaciens

<220>

<221> CDS

<222> (1)..(1269)

<223>

<400> 3

atg cag tct tct tca gct ctt cgg caa tca acc ggc gat cag tcg gaa	48
Met Gln Ser Ser Ser Ala Leu Arg Gln Ser Thr Gly Asp Gln Ser Glu	
1 5 10 15	
tac cat gcc cag tcg aat atg atc ggc tct agc ccg gcg gac ggt ttg	96
Tyr His Ala Gln Ser Asn Met Ile Gly Ser Ser Pro Ala Asp Gly Leu	
20 25 30	
ctc gca ttg ccg ctt ctg acc gtc gat ctt gcc gtc tat cgc ggt aat	144
Leu Ala Leu Pro Leu Leu Thr Val Asp Leu Ala Val Tyr Arg Gly Asn	
35 40 45	
cgg gat cgc ttt ctt gcg ctt gtc tcg gcc cat gga gcg aag gcg gct	192
Arg Asp Arg Phe Leu Ala Leu Val Ser Ala His Gly Ala Lys Ala Ala	
50 55 60	
cca cat gcc aag acg ccg atg tgc ccg gag atc gcg atc gat ctg att	240
Pro His Ala Lys Thr Pro Met Cys Pro Glu Ile Ala Ile Asp Leu Ile	
65 70 75 80	
gaa gcc ggt gcc tgg ggc gcg acg gtc gcc gat ctc ttc cag gcg gaa	288
Glu Ala Gly Ala Trp Gly Ala Thr Val Ala Asp Leu Phe Gln Ala Glu	
85 90 95	
gtc ctg ctc aag gcc ggc gtg tcg aac ata ttg atc gcc aac cag atc	336
Val Leu Leu Lys Ala Gly Val Ser Asn Ile Leu Ile Ala Asn Gln Ile	
100 105 110	
ggc gga ttg aca tcc gcc aga cgc cta cgc atg ctc gca gat gct ttt	384
Gly Gly Leu Thr Ser Ala Arg Arg Leu Arg Met Leu Ala Asp Ala Phe	
115 120 125	
ccg aaa gcc gag att atc tgc tgt gtc gat tct gtt cag gcc tcg gcc	432
Pro Lys Ala Glu Ile Ile Cys Cys Val Asp Ser Val Gln Ala Ser Ala	

130	135	140	
aat ctg gtt cag gcc ttt caa ggg cgt gtg gat gcc cca ttc aag gtc Asn Leu Val Gln Ala Phe Gln Gly Arg Val Asp Ala Pro Phe Lys Val 145 150 155 160			480
ttc atc gaa gtc ggt gtc ggc cgc act ggc gcc cgt acg ttg aat gtt Phe Ile Glu Val Gly Val Gly Arg Thr Gly Ala Arg Thr Leu Asn Val 165 170 175			528
gca aag gat atc atc gac acc atc tcg aca agt gca gaa atc gta ctg Ala Lys Asp Ile Ile Asp Thr Ile Ser Thr Ser Ala Glu Ile Val Leu 180 185 190			576
gcc ggt gtg tcg acc tat gaa ggc tcc gtc tcc ggg gaa acg tcg gaa Ala Gly Val Ser Thr Tyr Glu Gly Ser Val Ser Gly Glu Thr Ser Glu 195 200 205			624
gca ctc gat gca aac atg gcg gcc ctg ttc gat ctc ctg acc gac agt Ala Leu Asp Ala Asn Met Ala Ala Leu Phe Asp Leu Leu Thr Asp Ser 210 215 220			672
ctt gca tcg ata cgc gaa aaa gat ccc ggg cgc ccg cta acg gtt tca Leu Ala Ser Ile Arg Glu Lys Asp Pro Gly Arg Pro Leu Thr Val Ser 225 230 235 240			720
gcc ggc ggt tcg atc cat ttc gac cgc gtg ctc gcg gcg ctt gtg ccc Ala Gly Gly Ser Ile His Phe Asp Arg Val Leu Ala Ala Leu Val Pro 245 250 255			768
gtt tgc gag gcg gat ggc aat gcg acg ttg ttg ctg cgc agc ggc gcc Val Cys Glu Ala Asp Gly Asn Ala Thr Leu Leu Leu Arg Ser Gly Ala 260 265 270			816
atc ttc ttc tct gat cac ggt gta tat cag cgc ggt ttc cag gca gtc Ile Phe Phe Ser Asp His Gly Val Tyr Gln Arg Gly Phe Gln Ala Val 275 280 285			864
gac gcc cgc aac cta ctc gca tcc ggc aag gtt gtc ttc aag gca tcc Asp Ala Arg Asn Leu Leu Ala Ser Gly Lys Val Val Phe Lys Ala Ser 290 295 300			912
gag gca ttt cag ccc tca atg cga atc tgg gcg gag gtc atc tcc gtt Glu Ala Phe Gln Pro Ser Met Arg Ile Trp Ala Glu Val Ile Ser Val 305 310 315 320			960
cct gag ccg ggg ctg gcg atc gtc ggc atg ggc atg ccg gat gta tcg Pro Glu Pro Gly Leu Ala Ile Val Gly Met Gly Met Arg Asp Val Ser 325 330 335			1008
ttc gat cag gac ctg ccc gtg gcg ctt cgg ctc cat agg gac gga cat Phe Asp Gln Asp Leu Pro Val Ala Leu Arg Leu His Arg Asp Gly His 340 345 350			1056
ctg gtc gaa gct gat ctc tct tca tcc gcg aag gtc ggc aag ctc aat Leu Val Glu Ala Asp Leu Ser Ser Ser Ala Lys Val Gly Lys Leu Asn 355 360 365			1104
gac cag cat gcc ttc ttg tcc ttc ggg aac ggc agc agt ctg gca atc Asp Gln His Ala Phe Leu Ser Phe Gly Asn Gly Ser Ser Leu Ala Ile			1152



370                      375                      380  
 ggc gat gtc ata gaa ttc ggc atc tcg cat ccc tgc acg tgc ttc gat      1200  
 Gly Asp Val Ile Glu Phe Gly Ile Ser His Pro Cys Thr Cys Phe Asp  
 385                      390                      395                      400  
 cgc tgg cgc gtc ttt cac gga atc gat gga tca ggc cgg atc cag cgc      1248  
 Arg Trp Arg Val Phe His Gly Ile Asp Gly Ser Gly Arg Ile Gln Arg  
 405                      410                      415  
 atc tac aca acc ttc ttt cac tag      1272  
 Ile Tyr Thr Thr Phe Phe His  
 420  
  
 <210> 4  
  
 <211> 423  
  
 <212> PRT  
  
 <213> Agrobacterium tumefaciens  
  
  
  
 <400> 4  
  
 Met Gln Ser Ser Ser Ala Leu Arg Gln Ser Thr Gly Asp Gln Ser Glu  
 1                      5                      10                      15  
  
 Tyr His Ala Gln Ser Asn Met Ile Gly Ser Ser Pro Ala Asp Gly Leu  
 20                      25                      30  
  
 Leu Ala Leu Pro Leu Leu Thr Val Asp Leu Ala Val Tyr Arg Gly Asn  
 35                      40                      45  
  
 Arg Asp Arg Phe Leu Ala Leu Val Ser Ala His Gly Ala Lys Ala Ala  
 50                      55                      60  
  
 Pro His Ala Lys Thr Pro Met Cys Pro Glu Ile Ala Ile Asp Leu Ile  
 65                      70                      75                      80  
  
 Glu Ala Gly Ala Trp Gly Ala Thr Val Ala Asp Leu Phe Gln Ala Glu  
 85                      90                      95  
  
 Val Leu Leu Lys Ala Gly Val Ser Asn Ile Leu Ile Ala Asn Gln Ile  
 100                      105                      110  
  
 Gly Gly Leu Thr Ser Ala Arg Arg Leu Arg Met Leu Ala Asp Ala Phe  
 115                      120                      125  
  
 Pro Lys Ala Glu Ile Ile Cys Cys Val Asp Ser Val Gln Ala Ser Ala

130	135	140
Asn Leu Val Gln Ala Phe Gln Gly Arg Val Asp Ala Pro Phe Lys Val 145 150 155 160		
Phe Ile Glu Val Gly Val Gly Arg Thr Gly Ala Arg Thr Leu Asn Val 165 170 175		
Ala Lys Asp Ile Ile Asp Thr Ile Ser Thr Ser Ala Glu Ile Val Leu 180 185 190		
Ala Gly Val Ser Thr Tyr Glu Gly Ser Val Ser Gly Glu Thr Ser Glu 195 200 205		
Ala Leu Asp Ala Asn Met Ala Ala Leu Phe Asp Leu Leu Thr Asp Ser 210 215 220		
Leu Ala Ser Ile Arg Glu Lys Asp Pro Gly Arg Pro Leu Thr Val Ser 225 230 235 240		
Ala Gly Gly Ser Ile His Phe Asp Arg Val Leu Ala Ala Leu Val Pro 245 250 255		
Val Cys Glu Ala Asp Gly Asn Ala Thr Leu Leu Leu Arg Ser Gly Ala 260 265 270		
Ile Phe Phe Ser Asp His Gly Val Tyr Gln Arg Gly Phe Gln Ala Val 275 280 285		
Asp Ala Arg Asn Leu Leu Ala Ser Gly Lys Val Val Phe Lys Ala Ser 290 295 300		
Glu Ala Phe Gln Pro Ser Met Arg Ile Trp Ala Glu Val Ile Ser Val 305 310 315 320		
Pro Glu Pro Gly Leu Ala Ile Val Gly Met Gly Met Arg Asp Val Ser 325 330 335		
Phe Asp Gln Asp Leu Pro Val Ala Leu Arg Leu His Arg Asp Gly His 340 345 350		
Leu Val Glu Ala Asp Leu Ser Ser Ser Ala Lys Val Gly Lys Leu Asn 355 360 365		
Asp Gln His Ala Phe Leu Ser Phe Gly Asn Gly Ser Ser Leu Ala Ile		

370

375

380

Gly Asp Val Ile Glu Phe Gly Ile Ser His Pro Cys Thr Cys Phe Asp  
 385 390 395 400

Arg Trp Arg Val Phe His Gly Ile Asp Gly Ser Gly Arg Ile Gln Arg  
 405 410 415

Ile Tyr Thr Thr Phe Phe His  
 420

&lt;210&gt; 5

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide primer

&lt;400&gt; 5

cccttaatta atgacgacat ctgataatct tc

32

&lt;210&gt; 6

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide primer

&lt;400&gt; 6

tttcgcgcgcg cttagtgggtt atcgcgcgcgc

30

&lt;210&gt; 7

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

<220>

<223> oligonucleotide primer

<400> 7

cccgtacca tgacgacatc tgataatctt c

31

<210> 8

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide primer

<400> 8

cccttaatta atgcagtctt cttcagctct tc

32

<210> 9

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide primer

<400> 9

tttgcgccg cctagtgaag gaaggttgtagat

35

<210> 10

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide primer

<400> 10  
aatcatgac tatgcagtct ttttcagctc ttcg 34

<210> 11

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide primer

<400> 11  
tatagatctc tagtgaaaga aggttggtga gat 33

<210> 12

<211> 31

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 12  
gcgttaatta atgagttata ctgtcggtag c 31

<210> 13

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 13  
tatgcggccg cttagaggag cttgttaaca gg 32

<210> 14

<211> 2665

<212> DNA

<213> vector

<400> 14

```

gacgaaaggg cctcgtgata cgcctatfff tataggttaa tgtcatgata ataatggfff      60
cttagacgtc aggtggcact ttfcggggaa atgtgcgcgg aaccctatt tgtttatfff      120
tctaaataca ttcaaatatg tatccgctca tgagacaata accctgataa atgcttcaat      180
aatattgaaa aaggaagagt atgagtattc aacatttccg tgtcgccctt attccctfff      240
ttgcggcatt ttgccttccf gtttttgctc acccagaaac gctggtgaaa gtaaaagatg      300
ctgaagatca gttgggtgca cgagtggggt acatcgaaat ggatctcaac agcggtaaga      360
tccttgagag ttttcgcccc gaagaacggt ttccaatgat gagcactfff aaagttctgc      420
tatgtggcgc ggtattatcc cgtattgacg ccgggcaaga gcaactcggf cgcgcatac      480
actattctca gaatgacttg gttgagtact caccagtcac agaaaagcat cttacggatg      540
gcatgacagt aagagaatta tgcagtgtg ccataaccaf gagtgataac actgcggcca      600
acttacttct gacaacgatc ggaggaccga aggagctaac cgcttttttg cacaacatgg      660
gggatcatgt aactcgcctt gatcgttggg aaccggagct gaatgaagcc ataccaaacf      720
acgagcgtga caccacgatg cctgtagcaa tggcaacaac gttgcgcaaa ctattaactg      780
gcgaactact tactctagct tcccggaac aattaataga ctggatggag gcggataaag      840
ttgcaggacc acttctgcgc tcggcccttc cggctggctg gtttattgct gataaatctg      900
gagccggtga gcgtgggtct cgcggtatca ttgcagcact ggggccagat ggtaagccct      960
cccgatcgt agttatctac acgacgggga gtcaggcaac tatggatgaa cgaaatagac     1020
agatcgctga gatagggtcc tcaactgatta agcattggta actgtcagac caagtttact     1080
catatatact ttagattgat ttaaaacttc atttttaatt taaaaggatc taggtgaaga     1140
tcctttttga taatctcatg accaaaatcc cttaacgtga gttttcgffc cactgagcgt     1200
cagaccccgf agaaaagatc aaaggatctt ctfgagatcc tttttttctg cgcgtaatct     1260
gctgcttgca aacaaaaaaa ccaccgctac cagcggtggt ttgtttgccg gatcaagagc     1320
taccaactct ttttcgaag gtaactggct tcagcagagc gcagatacca aatactgtcc     1380
ttctagtgtg gccgtagtta ggccaccact tcaagaactc tgtagcaccg cctacatacc     1440
tcgctctgct aatcctgtta ccagtggctg ctgccagtg gataagtcg tgtcttaccg     1500
ggttggactc aagacgatag ttaccggata aggcgcagcg gtcgggctga acgggggggt     1560

```

cgtgcacaca gccagcttg gagcgaacga cctacaccga actgagatac ctacagcgtg 1620  
 agctatgaga aagcgccacg cttcccgaag ggagaaaggc ggacaggtat ccggtaaagcg 1680  
 gcagggctcgg aacaggagag cgcacgaggg agcttccagg gggaaacgcc tggatatcttt 1740  
 atagtcctgt cgggtttcgc cacctctgac ttgagcgtcg atttttgtga tgctcgtcag 1800  
 gggggcggag cctatggaaa aacgccagca acgcggcctt ttacaggttc ctggcctttt 1860  
 gctggccttt tgctcacatg ttctttcctg cgttatcccc tgattctgtg gataaccgta 1920  
 ttaccgcctt tgagtgaact gataccgctc gccgcagccg aacgaccgag cgcagcagat 1980  
 cagtgaagcga ggaagcggaa gagcgcccaa tacgcaaacc gcctctcccc gcgcgttggc 2040  
 cgattcatta atgcagctgg cacgacaggt ttcccgaact gaaagcgggc agtgagcgcga 2100  
 acgcaattaa tgtgagttag ctcaactcatt aggcacccca ggctttacac tttatgcttc 2160  
 cggctcgtat gttgtgtgga attgtgagcg gataacaatt tcacacagga aacagctatg 2220  
 accatgatta cgaattcgag gttaattaac cccgcggccg caagcttggc actggccgtc 2280  
 gttttacaac gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgacgca 2340  
 catccccctt tcgccagctg gcgtaatagc gaagaggccc gcaccgatcg cccttcccaa 2400  
 cagttgcgca gcctgaatgg cgaatggcgc ctgatgcggg attttctcct tacgcatctg 2460  
 tgccgtatctt cacaccgcat atgggtgact ctcaagtaca tctgctctga tgccgcatag 2520  
 ttaagccagc cccgacaccc gccaacaccc gctgacgcgc cctgacgggc ttgtctgctc 2580  
 ccggcatccg cttacagaca agctgtgacc gtctccggga gctgcatgtg tcagagggtt 2640  
 tcaccgtcat caccgaaacg cgcga 2665

<210> 15

<211> 3433

<212> DNA

<213> vector

<400> 15

ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60  
 attgtgagcg gataacaatt tcacacagaa ttcttaaaga ggagaaatta attaaccgcc 120  
 cggccgcgga tccagatctc atcaccatca ccatcactaa gcttaattag ctgagcttgg 180  
 actcctgttg atagatccag taatgacctc agaactccat ctggatttgt tcagaacgct 240  
 cggttgccgc cgggcgtttt ttatttgtga gaatccaagc tagcttggcg agattttcag 300

gagctaagga agctaaaatg gagaaaaaaa tcaactggata taccaccgtt gatatatccc	360
aatggcatcg taaagaacat tttgaggcat ttcagtcagt tgctcaatgt acctataacc	420
agaccgttca gctggatatt acggcctttt taaagaccgt aaagaaaaat aagcacaagt	480
tttatccggc ctttattcac attcttgccc gcctgatgaa tgctcatccg gaatttcgta	540
tggcaatgaa agacggtgag ctggtgatat gggatagtgt tcacccttgt tacaccgttt	600
tccatgagca aactgaaacg ttttcatcgc tctggagtga ataccacgac gatttcgggc	660
agtttctaca catatattcg caagatgtgg cgtgttacgg tgaaaacctg gcctatttcc	720
ctaaaggggtt tattgagaat atgtttttcg tctcagccaa tccctgggtg agtttcacca	780
gttttgattt aaacgtggcc aatatggaca acttcttcgc ccccgttttc accatgggca	840
aatattatac gcaaggcgac aaggtgctga tgccgctggc gattcagggt catcatgccg	900
tttgtgatgg cttccatgtc ggcagaatgc ttaatgaatt acaacagtac tgcgatgagt	960
ggcaggggcg ggcgtaattt ttttaaggca gttattgggt cccttaaacg cctggggtaa	1020
tgactctcta gcttgaggca tcaaataaaa cgaaaggctc agtcgaaaga ctgggccttt	1080
cgttttatct gttgtttgtc ggtgaacgct ctctgagta ggacaaatcc gccctctaga	1140
gctgcctcgc gcgtttcggt gatgacggtg aaaacctctg acacatgcag ctcccggaga	1200
cggtcacagc ttgtctgtaa gcggatgccg ggagcagaca agcccgtcag ggcgcgtcag	1260
cgggtgttgg cgggtgtcgg ggcgcagcca tgaccagtc acgtagcgat agcggagtgt	1320
atactggctt aactatgcgg catcagagca gattgtactg agagtgcacc atatgcggtg	1380
tgaaataccg cacagatgcg taaggagaaa ataccgcac aggcgctctt ccgcttcctc	1440
gctcactgac tcgctgcgct cggtcgttcg gctgcggcga gcggtatcag ctcaactcaa	1500
ggcggttaata cggttatcca cagaatcagg ggataacgca ggaaagaaca tgtgagcaaa	1560
aggccagcaa aaggccagga accgtaaaaa ggccgcgttg ctggcgtttt tccataggct	1620
ccgccccct gacgagcatc acaaaaatcg acgctcaagt cagaggtggc gaaacccgac	1680
aggactataa agataccagg cgtttcccc tggaagctcc ctctgctgct ctctgttcc	1740
gaccctgccg cttaccggat acctgtccgc ctttctccct tcgggaagcg tggcgctttc	1800
tcatagctca cgctgtaggt atctcagttc ggtgtaggtc gttcgtcca agctgggctg	1860
tgtgcacgaa cccccgttc agcccagcg ctgcgcctta tccggttaact atcgtcttga	1920
gtccaacccg gtaagacacg acttatcgcc actggcagca gccactggta acaggattag	1980
cagagcgagg tatgtaggcg gtgctacaga gttcttgaag tgggtggccta actacggcta	2040
cactagaagg acagtatttg gtatctgcgc tctgctgaag ccagttacct tcggaaaaag	2100



```

agttggtagc tcttgatccg gcaaacaaac caccgctggg agcgggtggt tttttgtttg 2160
caagcagcag attacgcgca gaaaaaaagg atctcaagaa gatcctttga tcttttctac 2220
ggggtctgac gctcagtggg acgaaaactc acgttaaggg attttgggtca tgagattatc 2280
aaaaaggatc ttcacctaga tccttttaaa ttaaaaatga agttttaaat caatctaaag 2340
tatatatgag taaacttggt ctgacagtta ccaatgctta atcagtgagg cacctatctc 2400
agcgatctgt ctatttcggt catccatagt tgccgtgactc cccgtcgtgt agataactac 2460
gatacgggag ggcttaccat ctggccccag tgctgcaatg ataccgcgag acccagctc 2520
accggctcca gatttatcag caataaacca gccagccgga agggccgagc gcagaagtgg 2580
tcctgcaact ttatccgcct ccatccagtc tattaattgt tgccgggaag ctagagtaa 2640
tagttcgcca gttaatagtt tgcgcaacgt tggtgccatt gctacaggca tcgtggtgtc 2700
acgctcgtcg tttggtatgg cttcattcag ctccggttcc caacgatcaa ggcgagttac 2760
atgatcccc atgttgtgca aaaaagcggg tagctccttc ggtcctccga tcgttgtcag 2820
aagtaagttg gccgcagtgt tatcactcat ggttatggca gactgcata attctcttac 2880
tgtcatgcca tccgtaagat gcttttctgt gactggtgag tactcaacca agtcattctg 2940
agaatagtgt atgcggcgac cgagttgctc ttgcccggcg tcaatacggg ataataccgc 3000
gccacatagc agaactttaa aagtgctcat cattggaaaa cgttcttcgg ggcgaaaact 3060
ctcaaggatc ttaccgctgt tgagatccag ttcgatgtaa cccactcgtg cacccaactg 3120
atcttcagca tcttttactt tcaccagcgt ttctgggtga gaaaaaacag gaaggcaaaa 3180
tgccgcaaaa aagggaataa gggcgacacg gaaatgttga atactcatac tcttcctttt 3240
tcaatattat tgaagcattt atcagggtta ttgtctcatg agcggataca tatttgaatg 3300
tatttagaaa aataaaciaa taggggttcc gcgcacattt ccccgaaaag tgccacctga 3360
cgtctaagaa accattatta tcatgacatt aacctataaa aataggcgta tcacgaggcc 3420
ctttcgtctt cac 3433

```

<210> 16

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 16

atatttaatt aatgtctgaa attactttgg

30

<210> 17

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 17

atatgcggcc gcttattgct tagcgttggt

30

<210> 18

<211> 1707

<212> DNA

<213> Zymomonas mobilis

<220>

<221> CDS

<222> (1)..(1707)

<223>

<400> 18

atg agt tat act gtc ggt acc tat tta gcg gag cgg ctt gtc cag att  
Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile  
1 5 10 15

48

ggt ctc aag cat cac ttc gca gtc gcg ggc gac tac aac ctc gtc ctt  
Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu  
20 25 30

96

ctt gac aac ctg ctt ttg aac aaa aac atg gag cag gtt tat tgc tgt  
Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys  
35 40 45

144

aac gaa ctg aac tgc ggt ttc agt gca gaa ggt tat gct cgt gcc aaa  
Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Lys  
50 55 60

192

ggc gca gca gca gcc gtc gtt acc tac agc gtc ggt gcg ctt tcc gca Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala 65 70 75 80	240
ttt gat gct atc ggt ggc gcc tat gca gaa aac ctt ccg gtt atc ctg Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu 85 90 95	288
atc tcc ggt gct ccg aac aac aat gat cac gct gct ggt cac gtg ttg Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu 100 105 110	336
cat cac gct ctt ggc aaa acc gac tat cac tat cag ttg gaa atg gcc His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala 115 120 125	384
aag aac atc acg gcc gcc gct gaa gcg att tac acc ccg gaa gaa gct Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala 130 135 140	432
ccg gct aaa atc gat cac gtg att aaa act gct ctt cgt gag aag aag Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys 145 150 155 160	480
ccg gtt tat ctc gaa atc gct tgc aac att gct tcc atg ccc tgc gcc Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala 165 170 175	528
gct cct gga ccg gca agc gca ttg ttc aat gac gaa gcc agc gac gaa Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu 180 185 190	576
gct tct ttg aat gca gcg gtt gaa gaa acc ctg aaa ttc atc gcc aac Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn 195 200 205	624
cgc gac aaa gtt gcc gtc ctc gtc ggc agc aag ctg cgc gca gct ggt Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly 210 215 220	672
gct gaa gaa gct gct gtc aaa ttt gct gat gct ctc ggt ggc gca gtt Ala Glu Glu Ala Ala Val Lys Phe Ala Asp Ala Leu Gly Gly Ala Val 225 230 235 240	720
gct acc atg gct gct gca aaa agc ttc ttc cca gaa gaa aac ccg cat Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His 245 250 255	768
tac atc ggc acc tca tgg ggt gaa gtc agc tat ccg ggc gtt gaa aag Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys 260 265 270	816
acg atg aaa gaa gcc gat gcg gtt atc gct ctg gct cct gtc ttc aac Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn 275 280 285	864
gac tac tcc acc act ggt tgg acg gat att cct gat cct aag aaa ctg Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu 290 295 300	912

gtt ctc gct gaa ccg cgt tct gtc gtc gtt aac ggc att cgc ttc ccc Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro 305 310 315 320	960
agc gtc cat ctg aaa gac tat ctg acc cgt ttg gct cag aaa gtt tcc Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser 325 330 335	1008
aag aaa acc ggt gca ttg gac ttc ttc aaa tcc ctc aat gca ggt gaa Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu 340 345 350	1056
ctg aag aaa gcc gct ccg gct gat ccg agt gct ccg ttg gtc aac gca Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala 355 360 365	1104
gaa atc gcc cgt cag gtc gaa gct ctt ctg acc ccg aac acg acg gtt Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val 370 375 380	1152
att gct gaa acc ggt gac tct tgg ttc aat gct cag cgc atg aag ctc Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu 385 390 395 400	1200
ccg aac ggt gct cgc gtt gaa tat gaa atg cag tgg ggt cac att ggt Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly 405 410 415	1248
tgg tcc gtt cct gcc gcc ttc ggt tat gcc gtc ggt gct ccg gaa cgt Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg 420 425 430	1296
cgc aac atc ctc atg gtt ggt gat ggt tcc ttc cag ctg acg gct cag Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln 435 440 445	1344
gaa gtc gct cag atg gtt cgc ctg aaa ctg ccg gtt atc atc ttc ttg Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu 450 455 460	1392
atc aat aac tat ggt tac acc atc gaa gtt atg atc cat gat ggt ccg Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro 465 470 475 480	1440
tac aac aac atc aag aac tgg gat tat gcc ggt ctg atg gaa gtg ttc Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe 485 490 495	1488
aac ggt aac ggt ggt tat gac agc ggt gct ggt aaa ggc ctg aag gct Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala 500 505 510	1536
aaa acc ggt ggc gaa ctg gca gaa gct atc aag gtt gct ctg gca aac Lys Thr Gly Gly Glu Leu Ala Ala Ile Lys Val Ala Leu Ala Asn 515 520 525	1584
acc gac ggc cca acc ctg atc gaa tgc ttc atc ggt cgt gaa gac tgc Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys 530 535 540	1632

act gaa gaa ttg gtc aaa tgg ggt aag cgc gtt gct gcc gcc aac agc 1680  
 Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser  
 545 550 555 560

cgt aag cct gtt aac aag ctc ctc tag 1707  
 Arg Lys Pro Val Asn Lys Leu Leu  
 565

<210> 19

<211> 568

<212> PRT

<213> Zymomonas mobilis

<400> 19

Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile  
 1 5 10 15

Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu  
 20 25 30

Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys  
 35 40 45

Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Lys  
 50 55 60

Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala  
 65 70 75 80

Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu  
 85 90 95

Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu  
 100 105 110

His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala  
 115 120 125

Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala  
 130 135 140

Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys  
 145 150 155 160

Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala  
165 170 175

Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu  
180 185 190

Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn  
195 200 205

Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly  
210 215 220

Ala Glu Glu Ala Ala Val Lys Phe Ala Asp Ala Leu Gly Gly Ala Val  
225 230 235 240

Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His  
245 250 255

Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys  
260 265 270

Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn  
275 280 285

Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu  
290 295 300

Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro  
305 310 315 320

Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser  
325 330 335

Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu  
340 345 350

Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala  
355 360 365

Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val  
370 375 380

Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu  
385 390 395 400

Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly  
                             405                            410                            415

Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg  
                             420                            425                            430

Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln  
                             435                            440                            445

Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu  
                             450                            455                            460

Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro  
                             465                            470                            475                            480

Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe  
                             485                            490                            495

Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala  
                             500                            505                            510

Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn  
                             515                            520                            525

Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys  
                             530                            535                            540

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser  
                             545                            550                            555                            560

Arg Lys Pro Val Asn Lys Leu Leu  
                             565

<210> 20

<211> 1692

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

&lt;222&gt; (1)..(1692)

&lt;223&gt;

&lt;400&gt; 20

atg tct gaa att act ttg ggt aaa tat ttg ttc gaa aga tta aag caa	48
Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln	
1 5 10 15	
gtc aac gtt aac acc gtt ttc ggt ttg cca ggt gac ttc aac ttg tcc	96
Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser	
20 25 30	
ttg ttg gac aag atc tac gaa gtt gaa ggt atg aga tgg gct ggt aac	144
Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn	
35 40 45	
gcc aac gaa ttg aac gct gct tac gcc gct gat ggt tac gct cgt atc	192
Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile	
50 55 60	
aag ggt atg tct tgt atc atc acc acc ttc ggt gtc ggt gaa ttg tct	240
Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser	
65 70 75 80	
gct ttg aac ggt att gcc ggt tct tac gct gaa cac gtc ggt gtt ttg	288
Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu	
85 90 95	
cac gtt gtt ggt gtc cca tcc atc tct gct caa gct aag caa ttg ttg	336
His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu	
100 105 110	
ttg cac cac acc ttg ggt aac ggt gac ttc act gtt ttc cac aga atg	384
Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met	
115 120 125	
tct gcc aac att tct gaa acc act gct atg atc act gac att gct acc	432
Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr	
130 135 140	
gcc cca gct gaa att gac aga tgt atc aga acc act tac gtc acc caa	480
Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln	
145 150 155 160	
aga cca gtc tac tta ggt ttg cca gct aac ttg gtc gac ttg aac gtc	528
Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val	
165 170 175	
cca gct aag ttg ttg caa act cca att gac atg tct ttg aag cca aac	576
Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn	
180 185 190	
gat gct gaa tcc gaa aag gaa gtc att gac acc atc ttg gct ttg gtc	624
Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val	
195 200 205	
aag gat gct aag aac cca gtt atc ttg gct gat gct tgt tgt tcc aga	672



Lys	Asp	Ala	Lys	Asn	Pro	Val	Ile	Leu	Ala	Asp	Ala	Cys	Cys	Ser	Arg	
210						215					220					
cac	gac	gtc	aag	gct	gaa	act	aag	aag	ttg	att	gac	ttg	act	caa	ttc	720
His	Asp	Val	Lys	Ala	Glu	Thr	Lys	Lys	Leu	Ile	Asp	Leu	Thr	Gln	Phe	
225					230				235						240	
cca	gct	ttc	gtc	acc	cca	atg	ggt	aag	ggt	tcc	att	gac	gaa	caa	cac	768
Pro	Ala	Phe	Val	Thr	Pro	Met	Gly	Lys	Gly	Ser	Ile	Asp	Glu	Gln	His	
				245					250						255	
cca	aga	tac	ggt	ggt	gtt	tac	gtc	ggt	acc	ttg	tcc	aag	cca	gaa	gtt	816
Pro	Arg	Tyr	Gly	Gly	Val	Tyr	Val	Gly	Thr	Leu	Ser	Lys	Pro	Glu	Val	
			260					265					270			
aag	gaa	gcc	gtt	gaa	tct	gct	gac	ttg	att	ttg	tct	gtc	ggt	gct	ttg	864
Lys	Glu	Ala	Val	Glu	Ser	Ala	Asp	Leu	Ile	Leu	Ser	Val	Gly	Ala	Leu	
		275					280					285				
ttg	tct	gat	ttc	aac	acc	ggt	tct	ttc	tct	tac	tct	tac	aag	acc	aag	912
Leu	Ser	Asp	Phe	Asn	Thr	Gly	Ser	Phe	Ser	Tyr	Ser	Tyr	Lys	Thr	Lys	
		290				295						300				
aac	att	gtc	gaa	ttc	cac	tcc	gac	cac	atg	aag	atc	aga	aac	gcc	act	960
Asn	Ile	Val	Glu	Phe	His	Ser	Asp	His	Met	Lys	Ile	Arg	Asn	Ala	Thr	
305					310					315					320	
ttc	cca	ggt	gtc	caa	atg	aaa	ttc	gtt	ttg	caa	aag	ttg	ttg	acc	act	1008
Phe	Pro	Gly	Val	Gln	Met	Lys	Phe	Val	Leu	Gln	Lys	Leu	Leu	Thr	Thr	
				325					330					335		
att	gct	gac	gcc	gct	aag	ggt	tac	aag	cca	gtt	gct	gtc	cca	gct	aga	1056
Ile	Ala	Asp	Ala	Ala	Lys	Gly	Tyr	Lys	Pro	Val	Ala	Val	Pro	Ala	Arg	
			340					345					350			
act	cca	gct	aac	gct	gct	gtc	cca	gct	tct	acc	cca	ttg	aag	caa	gaa	1104
Thr	Pro	Ala	Asn	Ala	Ala	Val	Pro	Ala	Ser	Thr	Pro	Leu	Lys	Gln	Glu	
			355				360					365				
tgg	atg	tgg	aac	caa	ttg	ggt	aac	ttc	ttg	caa	gaa	ggt	gat	gtt	gtc	1152
Trp	Met	Trp	Asn	Gln	Leu	Gly	Asn	Phe	Leu	Gln	Glu	Gly	Asp	Val	Val	
		370				375						380				
att	gct	gaa	acc	ggt	acc	tcc	gct	ttc	ggt	atc	aac	caa	acc	act	ttc	1200
Ile	Ala	Glu	Thr	Gly	Thr	Ser	Ala	Phe	Gly	Ile	Asn	Gln	Thr	Thr	Phe	
385					390					395					400	
cca	aac	aac	acc	tac	ggt	atc	tct	caa	gtc	tta	tgg	ggt	tcc	att	ggt	1248
Pro	Asn	Asn	Thr	Tyr	Gly	Ile	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	
				405					410					415		
ttc	acc	act	ggt	gct	acc	ttg	ggt	gct	gct	ttc	gct	gct	gaa	gaa	att	1296
Phe	Thr	Thr	Gly	Ala	Thr	Leu	Gly	Ala	Ala	Phe	Ala	Ala	Glu	Glu	Ile	
			420					425					430			
gat	cca	aag	aag	aga	gtt	atc	tta	ttc	att	ggt	gac	ggt	tct	ttg	caa	1344
Asp	Pro	Lys	Lys	Arg	Val	Ile	Leu	Phe	Ile	Gly	Asp	Gly	Ser	Leu	Gln	
		435					440					445				
ttg	act	gtt	caa	gaa	atc	tcc	acc	atg	atc	aga	tgg	ggc	ttg	aag	cca	1392

Leu	Thr	Val	Gln	Glu	Ile	Ser	Thr	Met	Ile	Arg	Trp	Gly	Leu	Lys	Pro		
450						455					460						
tac	ttg	ttc	gtc	ttg	aac	aac	gat	ggg	tac	acc	att	gaa	aag	ttg	att	1440	
Tyr	Leu	Phe	Val	Leu	Asn	Asn	Asp	Gly	Tyr	Thr	Ile	Glu	Lys	Leu	Ile		
465					470					475					480		
cac	ggg	cca	aag	gct	caa	tac	aac	gaa	att	caa	ggg	tg	gac	cac	cta	1488	
His	Gly	Pro	Lys	Ala	Gln	Tyr	Asn	Glu	Ile	Gln	Gly	Trp	Asp	His	Leu		
				485					490						495		
tcc	ttg	ttg	cca	act	ttc	ggg	gct	aag	gac	tat	gaa	acc	cac	aga	gtc	1536	
Ser	Leu	Leu	Pro	Thr	Phe	Gly	Ala	Lys	Asp	Tyr	Glu	Thr	His	Arg	Val		
			500					505						510			
gct	acc	acc	ggg	gaa	tg	gac	aag	ttg	acc	caa	gac	aag	tct	ttc	aac	1584	
Ala	Thr	Thr	Gly	Glu	Trp	Asp	Lys	Leu	Thr	Gln	Asp	Lys	Ser	Phe	Asn		
		515					520					525					
gac	aac	tct	aag	atc	aga	atg	att	gaa	atc	atg	ttg	cca	gtc	ttc	gat	1632	
Asp	Asn	Ser	Lys	Ile	Arg	Met	Ile	Glu	Ile	Met	Leu	Pro	Val	Phe	Asp		
	530					535					540						
gct	cca	caa	aac	ttg	gtt	gaa	caa	gct	aag	ttg	act	gct	gct	acc	aac	1680	
Ala	Pro	Gln	Asn	Leu	Val	Glu	Gln	Ala	Lys	Leu	Thr	Ala	Ala	Thr	Asn		
545					550					555					560		
gct	aag	caa	taa													1692	
Ala	Lys	Gln															

&lt;210&gt; 21

&lt;211&gt; 563

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 21

Met	Ser	Glu	Ile	Thr	Leu	Gly	Lys	Tyr	Leu	Phe	Glu	Arg	Leu	Lys	Gln		
1				5					10					15			
Val	Asn	Val	Asn	Thr	Val	Phe	Gly	Leu	Pro	Gly	Asp	Phe	Asn	Leu	Ser		
			20					25					30				
Leu	Leu	Asp	Lys	Ile	Tyr	Glu	Val	Glu	Gly	Met	Arg	Trp	Ala	Gly	Asn		
		35					40					45					
Ala	Asn	Glu	Leu	Asn	Ala	Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg	Ile		
50						55					60						

Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser  
65 70 75 80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu  
85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu  
100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met  
115 120 125

Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr  
130 135 140

Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln  
145 150 155 160

Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val  
165 170 175

Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn  
180 185 190

Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val  
195 200 205

Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Cys Ser Arg  
210 215 220

His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe  
225 230 235 240

Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Asp Glu Gln His  
245 250 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val  
260 265 270

Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu  
275 280 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys  
290 295 300

Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr  
 305 310 315 320

Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr  
 325 330 335

Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg  
 340 345 350

Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln Glu  
 355 360 365

Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val  
 370 375 380

Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe  
 385 390 395 400

Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly  
 405 410 415

Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile  
 420 425 430

Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln  
 435 440 445

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro  
 450 455 460

Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile  
 465 470 475 480

His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu  
 485 490 495

Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val  
 500 505 510

Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn  
 515 520 525

Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp  
 530 535 540

Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn  
 545                      550                      555                      560

Ala Lys Gln

<210> 22

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 22

tctttaatta atgggttgtc cgtcattcat ata

33

<210> 23

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 23

ctaaagcttt taggccagag tggtcttgcg cg

32

<210> 24

<211> 1674

<212> DNA

<213> Acetobacter pasteurianus

<220>

<221> CDS

<222> (1) .. (1674)

&lt;223&gt;

&lt;400&gt; 24

gtg acc tat act gtt ggc atg tat ctt gca gaa cgc ctt gta cag atc	48
Val Thr Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Val Gln Ile	
1 5 10 15	
ggg ctg aag cat cac ttc gcc gtg ggc ggc gac tac aat ctc gtt ctt	96
Gly Leu Lys His His Phe Ala Val Gly Gly Asp Tyr Asn Leu Val Leu	
20 25 30	
ctg gat cag ttg ctc ctc aac aag gac atg aaa cag atc tat tgc tgc	144
Leu Asp Gln Leu Leu Leu Asn Lys Asp Met Lys Gln Ile Tyr Cys Cys	
35 40 45	
aat gag ttg aac tgt ggc ttc agc gcg gaa ggc tac gcc cgt tct aac	192
Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ser Asn	
50 55 60	
ggg gct gcg gca gcg gtt gtc acc ttc agc gtt ggc gcc att tcc gcc	240
Gly Ala Ala Ala Ala Val Val Thr Phe Ser Val Gly Ala Ile Ser Ala	
65 70 75 80	
atg aac gcc ctc ggc ggc gcc tat gcc gaa aac ctg ccg gtt atc ctg	288
Met Asn Ala Leu Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu	
85 90 95	
att tcc ggc gcg ccc aac agc aat gat cag ggc aca ggt cat atc ctg	336
Ile Ser Gly Ala Pro Asn Ser Asn Asp Gln Gly Thr Gly His Ile Leu	
100 105 110	
cat cac aca atc ggc aag acg gat tac agc tac cag ctt gaa atg gcc	384
His His Thr Ile Gly Lys Thr Asp Tyr Ser Tyr Gln Leu Glu Met Ala	
115 120 125	
cgt cag gtc acc tgt gcc gcc gaa agc att acc gac gct cac tcc gcc	432
Arg Gln Val Thr Cys Ala Ala Glu Ser Ile Thr Asp Ala His Ser Ala	
130 135 140	
ccg gcc aag att gac cac gtc att cgc acg gcg ctg cgc gag cgt aag	480
Pro Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys	
145 150 155 160	
ccg gcc tat ctg gac atc gcg tgc aac att gcc tcc gag ccc tgc gtg	528
Pro Ala Tyr Leu Asp Ile Ala Cys Asn Ile Ala Ser Glu Pro Cys Val	
165 170 175	
cgg cct ggc cct gtc agc agc ctg ctg tcc gag cct gaa atc gac cac	576
Arg Pro Gly Pro Val Ser Ser Leu Leu Ser Glu Pro Glu Ile Asp His	
180 185 190	
acg agc ctg aag gcc gca gtg gac gcc acg gtt gcc ttg ctg aaa aat	624
Thr Ser Leu Lys Ala Ala Val Asp Ala Thr Val Ala Leu Leu Lys Asn	
195 200 205	
cgg cca gcc ccc gtc atg ctg ctg ggc agc aag ctg cgg gcc gcc aac	672
Arg Pro Ala Pro Val Met Leu Leu Gly Ser Lys Leu Arg Ala Ala Asn	
210 215 220	

gca ctg gcc gca acc gaa acg ctg gca gac aag ctg caa tgc gcg gtg Ala Leu Ala Ala Thr Glu Thr Leu Ala Asp Lys Leu Gln Cys Ala Val 225 230 235 240	720
acc atc atg gcg gcc gcg aaa ggc ttt ttc ccc gaa gac cac gcg ggt Thr Ile Met Ala Ala Ala Lys Gly Phe Phe Pro Glu Asp His Ala Gly 245 250 255	768
ttc cgc ggc ctg tac tgg ggc gaa gtc tcg aac ccc ggc gtg cag gaa Phe Arg Gly Leu Tyr Trp Gly Glu Val Ser Asn Pro Gly Val Gln Glu 260 265 270	816
ctg gtg gag acc tcc gac gca ctg ctg tgc atc gcc ccc gta ttc aac Leu Val Glu Thr Ser Asp Ala Leu Leu Cys Ile Ala Pro Val Phe Asn 275 280 285	864
gac tat tca aca gtc ggc tgg tcg ggc atg ccc aag ggc ccc aat gtg Asp Tyr Ser Thr Val Gly Trp Ser Gly Met Pro Lys Gly Pro Asn Val 290 295 300	912
att ctg gct gag ccc gac cgc gta acg gtc gat ggc cgc gcc tat gac Ile Leu Ala Glu Pro Asp Arg Val Thr Val Asp Gly Arg Ala Tyr Asp 305 310 315 320	960
ggc ttt acc ctg cgc gcc ttc ctg cag gct ctg gcg gaa aaa gcc ccc Gly Phe Thr Leu Arg Ala Phe Leu Gln Ala Leu Ala Glu Lys Ala Pro 325 330 335	1008
gcg cgc ccg gcc tcc gca cag aaa agc agc gtc ccg acg tgc tcg ctc Ala Arg Pro Ala Ser Ala Gln Lys Ser Ser Val Pro Thr Cys Ser Leu 340 345 350	1056
acc gcg aca tcc gat gaa gcc ggt ctg acg aat gac gaa atc gtc cgt Thr Ala Thr Ser Asp Glu Ala Gly Leu Thr Asn Asp Glu Ile Val Arg 355 360 365	1104
cat atc aac gcc ctg ctg aca tca aac acg acg ctg gtg gca gaa acc His Ile Asn Ala Leu Leu Thr Ser Asn Thr Thr Leu Val Ala Glu Thr 370 375 380	1152
ggc gat tca tgg ttc aat gcc atg cgc atg acc ctg gcc ggt gcg cgc Gly Asp Ser Trp Phe Asn Ala Met Arg Met Thr Leu Ala Gly Ala Arg 385 390 395 400	1200
gtg gaa ctg gaa atg cag tgg ggc cat atc ggc tgg tcc gtg ccc tcc Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser 405 410 415	1248
gcg ttc ggc aat gcc atg ggc tcg cag gac cgc cag cat gtg gtg atg Ala Phe Gly Asn Ala Met Gly Ser Gln Asp Arg Gln His Val Val Met 420 425 430	1296
gta ggc gat ggc tcc ttc cag ctt acc gcg cag gaa gtg gct cag atg Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met 435 440 445	1344
gtg cgc tac gaa ctg ccc gtc att atc ttt ctg atc aac aac cgt ggc Val Arg Tyr Glu Leu Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly 450 455 460	1392

tat gtc att gaa atc gcc att cat gac ggc ccg tac aac tat atc aag 1440  
 Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys  
 465 470 475 480

aac tgg gat tac gcc ggc ctg atg gaa gtc ttc aac gcc gga gaa ggc 1488  
 Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe Asn Ala Gly Glu Gly  
 485 490 495

cat gga ctt ggc ctg aaa gcc acc acc ccg aag gaa ctg aca gaa gcc 1536  
 His Gly Leu Gly Leu Lys Ala Thr Thr Pro Lys Glu Leu Thr Glu Ala  
 500 505 510

atc gcc agg gca aaa gcc aat acc cgc ggc ccg acg ctg atc gaa tgc 1584  
 Ile Ala Arg Ala Lys Ala Asn Thr Arg Gly Pro Thr Leu Ile Glu Cys  
 515 520 525

cag atc gac cgc acg gac tgc acg gat atg ctg gtt caa tgg ggc cgc 1632  
 Gln Ile Asp Arg Thr Asp Cys Thr Asp Met Leu Val Gln Trp Gly Arg  
 530 535 540

aag gtt gcc tca acc aac gcg cgc aag acc act ctg gcc tga 1674  
 Lys Val Ala Ser Thr Asn Ala Arg Lys Thr Thr Leu Ala  
 545 550 555

<210> 25

<211> 557

<212> PRT

<213> *Acetobacter pasteurianus*

<400> 25

Val Thr Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Val Gln Ile  
 1 5 10 15

Gly Leu Lys His His Phe Ala Val Gly Gly Asp Tyr Asn Leu Val Leu  
 20 25 30

Leu Asp Gln Leu Leu Leu Asn Lys Asp Met Lys Gln Ile Tyr Cys Cys  
 35 40 45

Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ser Asn  
 50 55 60

Gly Ala Ala Ala Ala Val Val Thr Phe Ser Val Gly Ala Ile Ser Ala  
 65 70 75 80

Met Asn Ala Leu Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu  
 85 90 95



Ile Ser Gly Ala Pro Asn Ser Asn Asp Gln Gly Thr Gly His Ile Leu  
 100 105 110

His His Thr Ile Gly Lys Thr Asp Tyr Ser Tyr Gln Leu Glu Met Ala  
 115 120 125

Arg Gln Val Thr Cys Ala Ala Glu Ser Ile Thr Asp Ala His Ser Ala  
 130 135 140

Pro Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys  
 145 150 155 160

Pro Ala Tyr Leu Asp Ile Ala Cys Asn Ile Ala Ser Glu Pro Cys Val  
 165 170 175

Arg Pro Gly Pro Val Ser Ser Leu Leu Ser Glu Pro Glu Ile Asp His  
 180 185 190

Thr Ser Leu Lys Ala Ala Val Asp Ala Thr Val Ala Leu Leu Lys Asn  
 195 200 205

Arg Pro Ala Pro Val Met Leu Leu Gly Ser Lys Leu Arg Ala Ala Asn  
 210 215 220

Ala Leu Ala Ala Thr Glu Thr Leu Ala Asp Lys Leu Gln Cys Ala Val  
 225 230 235 240

Thr Ile Met Ala Ala Ala Lys Gly Phe Phe Pro Glu Asp His Ala Gly  
 245 250 255

Phe Arg Gly Leu Tyr Trp Gly Glu Val Ser Asn Pro Gly Val Gln Glu  
 260 265 270

Leu Val Glu Thr Ser Asp Ala Leu Leu Cys Ile Ala Pro Val Phe Asn  
 275 280 285

Asp Tyr Ser Thr Val Gly Trp Ser Gly Met Pro Lys Gly Pro Asn Val  
 290 295 300

Ile Leu Ala Glu Pro Asp Arg Val Thr Val Asp Gly Arg Ala Tyr Asp  
 305 310 315 320

Gly Phe Thr Leu Arg Ala Phe Leu Gln Ala Leu Ala Glu Lys Ala Pro  
 325 330 335

Ala Arg Pro Ala Ser Ala Gln Lys Ser Ser Val Pro Thr Cys Ser Leu  
 340 345 350

Thr Ala Thr Ser Asp Glu Ala Gly Leu Thr Asn Asp Glu Ile Val Arg  
 355 360 365

His Ile Asn Ala Leu Leu Thr Ser Asn Thr Thr Leu Val Ala Glu Thr  
 370 375 380

Gly Asp Ser Trp Phe Asn Ala Met Arg Met Thr Leu Ala Gly Ala Arg  
 385 390 395 400

Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser  
 405 410 415

Ala Phe Gly Asn Ala Met Gly Ser Gln Asp Arg Gln His Val Val Met  
 420 425 430

Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met  
 435 440 445

Val Arg Tyr Glu Leu Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly  
 450 455 460

Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys  
 465 470 475 480

Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe Asn Ala Gly Glu Gly  
 485 490 495

His Gly Leu Gly Leu Lys Ala Thr Thr Pro Lys Glu Leu Thr Glu Ala  
 500 505 510

Ile Ala Arg Ala Lys Ala Asn Thr Arg Gly Pro Thr Leu Ile Glu Cys  
 515 520 525

Gln Ile Asp Arg Thr Asp Cys Thr Asp Met Leu Val Gln Trp Gly Arg  
 530 535 540

Lys Val Ala Ser Thr Asn Ala Arg Lys Thr Thr Leu Ala  
 545 550 555

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 26

atcttaatta atgtataccg ttggtatgta ct

32

<210> 27

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 27

tatgcggccg cttacgcttg tggtttgcga gagt

34

<210> 28

<211> 1671

<212> DNA

<213> Zymobacter palmae

<220>

<221> CDS

<222> (1)..(1671)

<223>

<400> 28

atg tat acc gtt ggt atg tac ttg gca gaa cgc cta gcc cag atc ggc  
Met Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Ala Gln Ile Gly  
1 5 10 15

48

ctg aaa cac cac ttt gcc gtg gcc ggt gac tac aac ctg gtg ttg ctt

96

Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu	Leu	
			20					25					30			
gat	cag	ctc	ctg	ctg	aac	aaa	gac	atg	gag	cag	gtc	tac	tgc	tgt	aac	144
Asp	Gln	Leu	Leu	Leu	Asn	Lys	Asp	Met	Glu	Gln	Val	Tyr	Cys	Cys	Asn	
		35					40					45				
gaa	ctt	aac	tgc	ggc	ttt	agc	gcc	gaa	ggt	tac	gct	cgt	gca	cgt	ggt	192
Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Arg	Gly	
	50					55					60					
gcc	gcc	gct	gcc	atc	gtc	acg	ttc	agc	gta	ggt	gct	atc	tct	gca	atg	240
Ala	Ala	Ala	Ala	Ile	Val	Thr	Phe	Ser	Val	Gly	Ala	Ile	Ser	Ala	Met	
65					70					75					80	
aac	gcc	atc	ggt	ggc	gcc	tat	gca	gaa	aac	ctg	ccg	gtc	atc	ctg	atc	288
Asn	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu	Ile	
			85						90					95		
tct	ggc	tca	ccg	aac	acc	aat	gac	tac	ggc	aca	ggc	cac	atc	ctg	cac	336
Ser	Gly	Ser	Pro	Asn	Thr	Asn	Asp	Tyr	Gly	Thr	Gly	His	Ile	Leu	His	
			100					105					110			
cac	acc	att	ggt	act	act	gac	tat	aac	tat	cag	ctg	gaa	atg	gta	aaa	384
His	Thr	Ile	Gly	Thr	Thr	Asp	Tyr	Asn	Tyr	Gln	Leu	Glu	Met	Val	Lys	
		115					120					125				
cac	gtt	acc	tgc	gca	cgt	gaa	agc	atc	gtt	tct	gcc	gaa	gaa	gca	ccg	432
His	Val	Thr	Cys	Ala	Arg	Glu	Ser	Ile	Val	Ser	Ala	Glu	Glu	Ala	Pro	
	130					135					140					
gca	aaa	atc	gac	cac	gtc	atc	cgt	acg	gct	cta	cgt	gaa	cgc	aaa	ccg	480
Ala	Lys	Ile	Asp	His	Val	Ile	Arg	Thr	Ala	Leu	Arg	Glu	Arg	Lys	Pro	
145					150					155					160	
gct	tat	ctg	gaa	atc	gca	tgc	aac	gtc	gct	ggc	gct	gaa	tgt	gtt	cgt	528
Ala	Tyr	Leu	Glu	Ile	Ala	Cys	Asn	Val	Ala	Gly	Ala	Glu	Cys	Val	Arg	
			165					170						175		
ccg	ggc	ccg	atc	aat	agc	ctg	ctg	cgt	gaa	ctc	gaa	gtt	gac	cag	acc	576
Pro	Gly	Pro	Ile	Asn	Ser	Leu	Leu	Arg	Glu	Leu	Glu	Val	Asp	Gln	Thr	
			180					185					190			
agt	gtc	act	gcc	gct	gta	gat	gcc	gcc	gta	gaa	tggt	ctg	cag	gac	cgc	624
Ser	Val	Thr	Ala	Ala	Val	Asp	Ala	Ala	Val	Glu	Trp	Leu	Gln	Asp	Arg	
		195					200					205				
cag	aac	gtc	gtc	atg	ctg	gtc	ggt	agc	aaa	ctg	cgt	gcc	gct	gcc	gct	672
Gln	Asn	Val	Val	Met	Leu	Val	Gly	Ser	Lys	Leu	Arg	Ala	Ala	Ala	Ala	
	210					215					220					
gaa	aaa	cag	gct	gtt	gcc	cta	gcg	gac	cgc	ctg	ggc	tgc	gct	gtc	acg	720
Glu	Lys	Gln	Ala	Val	Ala	Leu	Ala	Asp	Arg	Leu	Gly	Cys	Ala	Val	Thr	
225					230					235					240	
atc	atg	gct	gcc	gaa	aaa	ggc	ttc	ttc	ccg	gaa	gat	cat	ccg	aac	ttc	768
Ile	Met	Ala	Ala	Glu	Lys	Gly	Phe	Phe	Pro	Glu	Asp	His	Pro	Asn	Phe	
			245						250					255		
cgc	ggc	ctg	tac	tgg	ggt	gaa	gtc	agc	tcc	gaa	ggt	gca	cag	gaa	ctg	816

Arg	Gly	Leu	Tyr	Trp	Gly	Glu	Val	Ser	Ser	Glu	Gly	Ala	Gln	Glu	Leu	
			260					265					270			
gtt	gaa	aac	gcc	gat	gcc	atc	ctg	tgt	ctg	gca	ccg	gta	ttc	aac	gac	864
Val	Glu	Asn	Ala	Asp	Ala	Ile	Leu	Cys	Leu	Ala	Pro	Val	Phe	Asn	Asp	
		275					280					285				
tat	gct	acc	gtt	ggc	tgg	aac	tcc	tgg	ccg	aaa	ggc	gac	aat	gtc	atg	912
Tyr	Ala	Thr	Val	Gly	Trp	Asn	Ser	Trp	Pro	Lys	Gly	Asp	Asn	Val	Met	
	290					295					300					
gtc	atg	gac	acc	gac	cgc	gtc	act	ttc	gca	gga	cag	tcc	ttc	gaa	ggc	960
Val	Met	Asp	Thr	Asp	Arg	Val	Thr	Phe	Ala	Gly	Gln	Ser	Phe	Glu	Gly	
305					310					315					320	
ctg	tca	ttg	agc	acc	ttc	gcc	gca	gca	ctg	gct	gag	aaa	gca	cct	tct	1008
Leu	Ser	Leu	Ser	Thr	Phe	Ala	Ala	Ala	Leu	Ala	Glu	Lys	Ala	Pro	Ser	
			325						330					335		
cgc	ccg	gca	acg	act	caa	ggc	act	caa	gca	ccg	gta	ctg	ggc	att	gag	1056
Arg	Pro	Ala	Thr	Thr	Gln	Gly	Thr	Gln	Ala	Pro	Val	Leu	Gly	Ile	Glu	
			340				345						350			
gcc	gca	gag	ccc	aat	gca	ccg	ctg	acc	aat	gac	gaa	atg	acg	cgt	cag	1104
Ala	Ala	Glu	Pro	Asn	Ala	Pro	Leu	Thr	Asn	Asp	Glu	Met	Thr	Arg	Gln	
		355					360					365				
atc	cag	tcg	ctg	atc	act	tcc	gac	act	act	ctg	aca	gca	gaa	aca	ggc	1152
Ile	Gln	Ser	Leu	Ile	Thr	Ser	Asp	Thr	Thr	Leu	Ala	Glu	Thr	Gly		
	370					375					380					
gac	tct	tgg	ttc	aac	gct	tct	cgc	atg	ccg	att	cct	ggc	ggc	gct	cgt	1200
Asp	Ser	Trp	Phe	Asn	Ala	Ser	Arg	Met	Pro	Ile	Pro	Gly	Gly	Ala	Arg	
385					390					395					400	
gtc	gaa	ctg	gaa	atg	caa	tgg	ggc	cat	atc	ggc	tgg	tcc	gta	cct	tct	1248
Val	Glu	Leu	Glu	Met	Gln	Trp	Gly	His	Ile	Gly	Trp	Ser	Val	Pro	Ser	
			405						410					415		
gca	ttc	ggc	aac	gcc	gtt	ggc	tct	ccg	gag	cgt	cgc	cac	atc	atg	atg	1296
Ala	Phe	Gly	Asn	Ala	Val	Gly	Ser	Pro	Glu	Arg	Arg	His	Ile	Met	Met	
			420					425					430			
gtc	ggc	gat	ggc	tct	ttc	cag	ctg	act	gct	caa	gaa	gtt	gct	cag	atg	1344
Val	Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Val	Ala	Gln	Met	
		435					440					445				
atc	cgc	tat	gaa	atc	ccg	gtc	atc	atc	ttc	ctg	atc	aac	aac	cgc	ggc	1392
Ile	Arg	Tyr	Glu	Ile	Pro	Val	Ile	Ile	Phe	Leu	Ile	Asn	Asn	Arg	Gly	
	450					455					460					
tac	gtc	atc	gaa	atc	gct	atc	cat	gac	ggc	cct	tac	aac	tac	atc	aaa	1440
Tyr	Val	Ile	Glu	Ile	Ala	Ile	His	Asp	Gly	Pro	Tyr	Asn	Tyr	Ile	Lys	
465					470					475					480	
aac	tgg	aac	tac	gct	ggc	ctg	atc	gac	gtc	ttc	aat	gac	gaa	gat	ggc	1488
Asn	Trp	Asn	Tyr	Ala	Gly	Leu	Ile	Asp	Val	Phe	Asn	Asp	Glu	Asp	Gly	
			485						490					495		
cat	ggc	ctg	ggc	ctg	aaa	gct	tct	act	ggc	gca	gaa	cta	gaa	ggc	gct	1536

His Gly Leu Gly Leu Lys Ala Ser Thr Gly Ala Glu Leu Glu Gly Ala  
 500 505 510  
 atc aag aaa gca ctc gac aat cgt cgc ggt ccg acg ctg atc gaa tgt 1584  
 Ile Lys Lys Ala Leu Asp Asn Arg Arg Gly Pro Thr Leu Ile Glu Cys  
 515 520 525  
 aac atc gct cag gac gac tgc act gaa acc ctg att gct tgg ggt aaa 1632  
 Asn Ile Ala Gln Asp Asp Cys Thr Glu Thr Leu Ile Ala Trp Gly Lys  
 530 535 540  
 cgt gta gca gct acc aac tct cgc aaa cca caa gcg taa 1671  
 Arg Val Ala Ala Thr Asn Ser Arg Lys Pro Gln Ala  
 545 550 555

<210> 29

<211> 556

<212> PRT

<213> Zymobacter palmae

<400> 29

Met Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Ala Gln Ile Gly  
 1 5 10 15  
 Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu Leu  
 20 25 30  
 Asp Gln Leu Leu Leu Asn Lys Asp Met Glu Gln Val Tyr Cys Cys Asn  
 35 40 45  
 Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Arg Gly  
 50 55 60  
 Ala Ala Ala Ala Ile Val Thr Phe Ser Val Gly Ala Ile Ser Ala Met  
 65 70 75 80  
 Asn Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu Ile  
 85 90 95  
 Ser Gly Ser Pro Asn Thr Asn Asp Tyr Gly Thr Gly His Ile Leu His  
 100 105 110  
 His Thr Ile Gly Thr Thr Asp Tyr Asn Tyr Gln Leu Glu Met Val Lys  
 115 120 125

His Val Thr Cys Ala Arg Glu Ser Ile Val Ser Ala Glu Glu Ala Pro  
 130 135 140

Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys Pro  
 145 150 155 160

Ala Tyr Leu Glu Ile Ala Cys Asn Val Ala Gly Ala Glu Cys Val Arg  
 165 170 175

Pro Gly Pro Ile Asn Ser Leu Leu Arg Glu Leu Glu Val Asp Gln Thr  
 180 185 190

Ser Val Thr Ala Ala Val Asp Ala Ala Val Glu Trp Leu Gln Asp Arg  
 195 200 205

Gln Asn Val Val Met Leu Val Gly Ser Lys Leu Arg Ala Ala Ala Ala  
 210 215 220

Glu Lys Gln Ala Val Ala Leu Ala Asp Arg Leu Gly Cys Ala Val Thr  
 225 230 235 240

Ile Met Ala Ala Glu Lys Gly Phe Phe Pro Glu Asp His Pro Asn Phe  
 245 250 255

Arg Gly Leu Tyr Trp Gly Glu Val Ser Ser Glu Gly Ala Gln Glu Leu  
 260 265 270

Val Glu Asn Ala Asp Ala Ile Leu Cys Leu Ala Pro Val Phe Asn Asp  
 275 280 285

Tyr Ala Thr Val Gly Trp Asn Ser Trp Pro Lys Gly Asp Asn Val Met  
 290 295 300

Val Met Asp Thr Asp Arg Val Thr Phe Ala Gly Gln Ser Phe Glu Gly  
 305 310 315 320

Leu Ser Leu Ser Thr Phe Ala Ala Ala Leu Ala Glu Lys Ala Pro Ser  
 325 330 335

Arg Pro Ala Thr Thr Gln Gly Thr Gln Ala Pro Val Leu Gly Ile Glu  
 340 345 350

Ala Ala Glu Pro Asn Ala Pro Leu Thr Asn Asp Glu Met Thr Arg Gln  
 355 360 365

Ile Gln Ser Leu Ile Thr Ser Asp Thr Thr Leu Thr Ala Glu Thr Gly  
 370 375 380

Asp Ser Trp Phe Asn Ala Ser Arg Met Pro Ile Pro Gly Gly Ala Arg  
 385 390 395 400

Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser  
 405 410 415

Ala Phe Gly Asn Ala Val Gly Ser Pro Glu Arg Arg His Ile Met Met  
 420 425 430

Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met  
 435 440 445

Ile Arg Tyr Glu Ile Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly  
 450 455 460

Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys  
 465 470 475 480

Asn Trp Asn Tyr Ala Gly Leu Ile Asp Val Phe Asn Asp Glu Asp Gly  
 485 490 495

His Gly Leu Gly Leu Lys Ala Ser Thr Gly Ala Glu Leu Glu Gly Ala  
 500 505 510

Ile Lys Lys Ala Leu Asp Asn Arg Arg Gly Pro Thr Leu Ile Glu Cys  
 515 520 525

Asn Ile Ala Gln Asp Asp Cys Thr Glu Thr Leu Ile Ala Trp Gly Lys  
 530 535 540

Arg Val Ala Ala Thr Asn Ser Arg Lys Pro Gln Ala  
 545 550 555

<210> 30

<211> 32

<212> DNA

<213> artificial sequence

<400> 30

ctattaatta atggcttcgg tacacggcac ca



<210> 31

<211> 34

<212> . DNA

<213> artificial sequence

<400> 31

tatgcggccg cttacttcac cgggcttacg gtgc

34

<210> 32

<211> 1587

<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (1) .. (1584)

<223>

<400> 32

atg gct tcg gta cac ggc acc aca tac gaa ctc ttg cga cgt caa ggc  
Met Ala Ser Val His Gly Thr Thr Tyr Glu Leu Leu Arg Arg Gln Gly  
1 5 10 15

48

atc gat acg gtc ttc ggc aat cct ggc tcg aac gag ctc ccg ttt ttg  
Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu  
20 25 30

96

aag gac ttt cca gag gac ttt cga tac atc ctg gct ttg cag gaa gcg  
Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala  
35 40 45

144

tgt	gtg	gtg	ggc	att	gca	gac	ggc	tat	gcg	caa	gcc	agt	cgg	aag	ccg
Cys	Val	Val	Gly	Ile	Ala	Asp	Gly	Tyr	Ala	Gln	Ala	Ser	Arg	Lys	Pro
50			55				60								

192

gct ttc att aac ctg cat tct gct gct ggt acc ggc aat gct atg ggt  
Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly  
65 70 75 80

240

gca ctc agt aac gcc tgg aac tca cat tcc ccg ctg atc gtc act gcc  
Ala Leu Ser Asn Ala Trp Asn Ser His Ser Pro Leu Ile Val Thr Ala  
85 90 95

288

ggc cag cag acc agg gcg atg att ggc gtt gaa gct ctg ctg acc aac Gly Gln Gln Thr Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn 100 105 110	336
gtc gat gcc gcc aac ctg cca cga cca ctt gtc aaa tgg agc tac gag Val Asp Ala Ala Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu 115 120 125	384
ccc gca agc gca gca gaa gtc cct cat gcg atg agc agg gct atc cat Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His 130 135 140	432
atg gca agc atg gcg cca caa ggc cct gtc tat ctt tcg gtg cca tat Met Ala Ser Met Ala Pro Gln Gly Pro Val Tyr Leu Ser Val Pro Tyr 145 150 155 160	480
gac gat tgg gat aag gat gct gat cct cag tcc cac cac ctt ttt gat Asp Asp Trp Asp Lys Asp Ala Asp Pro Gln Ser His His Leu Phe Asp 165 170 175	528
cgc cat gtc agt tca tca gta cgc ctg aac gac cag gat ctc gat att Arg His Val Ser Ser Ser Val Arg Leu Asn Asp Gln Asp Leu Asp Ile 180 185 190	576
ctg gtg aaa gct ctc aac agc gca tcc aac ccg gcg atc gtc ctg ggc Leu Val Lys Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly 195 200 205	624
ccg gac gtc gac gca gca aat gcg aac gca gac tgc gtc atg ttg gcc Pro Asp Val Asp Ala Ala Asn Ala Asn Ala Asp Cys Val Met Leu Ala 210 215 220	672
gaa cgc ctc aaa gct ccg gtt tgg gtt gcg cca tcc gct cca cgc tgc Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys 225 230 235 240	720
cca ttc cct acc cgt cat cct tgc ttc cgt gga ttg atg cca gct ggc Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly 245 250 255	768
atc gca gcg att tct cag ctg ctc gaa ggt cac gat gtg gtt ttg gta Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val 260 265 270	816
atc ggc gct cca gtg ttc cgt tac cac caa tac gac cca ggt caa tat Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr 275 280 285	864
ctc aaa cct ggc acg cga ttg att tcg gtg acc tgc gac ccg ctc gaa Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu 290 295 300	912
gct gca cgc gcg cca atg ggc gat gcg atc gtg gca gac att ggt gcg Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala 305 310 315 320	960
atg gct agc gct ctt gcc aac ttg gtt gaa gag agc agc cgc cag ctc Met Ala Ser Ala Leu Ala Asn Leu Val Glu Glu Ser Ser Arg Gln Leu 325 330 335	1008

cca act gca gct ccg gaa ccc gcg aag gtt gac caa gac gct ggc cga Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg 340 345 350	1056
ctt cac cca gag aca gtg ttc gac aca ctg aac gac atg gcc ccg gag Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu 355 360 365	1104
aat gcg att tac ctg aac gag tcg act tca acg acc gcc caa atg tgg Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Thr Ala Gln Met Trp 370 375 380	1152
cag cgc ctg aac atg cgc aac cct ggt agc tac tac ttc tgt gca gct Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala 385 390 395 400	1200
ggc gga ctg ggc ttc gcc ctg cct gca gca att ggc gtt caa ctc gca Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala 405 410 415	1248
gaa ccc gag cga caa gtc atc gcc gtc att ggc gac gga tcg gcg aac Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn 420 425 430	1296
tac agc att agt gcg ttg tgg act gca gct cag tac aac atc ccc act Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr 435 440 445	1344
atc ttc gtg atc atg aac aac ggc acc tac ggt gcg ttg cga tgg ttt Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe 450 455 460	1392
gcc ggc gtt ctc gaa gca gaa aac gtt cct ggg ctg gat gtg cca ggg Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly 465 470 475 480	1440
atc gac ttc cgc gca ctc gcc aag ggc tat ggt gtc caa gcg ctg aaa Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys 485 490 495	1488
gcc gac aac ctt gag cag ctc aag ggt tcg cta caa gaa gcg ctt tct Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser 500 505 510	1536
gcc aaa ggc ccg gta ctt atc gaa gta agc acc gta agc ccg gtg aag Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Pro Val Lys 515 520 525	1584
tga	1587

&lt;210&gt; 33

&lt;211&gt; 528

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas putida

&lt;400&gt; 33

Met Ala Ser Val His Gly Thr Thr Tyr Glu Leu Leu Arg Arg Gln Gly  
 1 5 10 15

Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu  
 20 25 30

Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala  
 35 40 45

Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro  
 50 55 60

Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly  
 65 70 75 80

Ala Leu Ser Asn Ala Trp Asn Ser His Ser Pro Leu Ile Val Thr Ala  
 85 90 95

Gly Gln Gln Thr Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn  
 100 105 110

Val Asp Ala Ala Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu  
 115 120 125

Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His  
 130 135 140

Met Ala Ser Met Ala Pro Gln Gly Pro Val Tyr Leu Ser Val Pro Tyr  
 145 150 155 160

Asp Asp Trp Asp Lys Asp Ala Asp Pro Gln Ser His His Leu Phe Asp  
 165 170 175

Arg His Val Ser Ser Ser Val Arg Leu Asn Asp Gln Asp Leu Asp Ile  
 180 185 190

Leu Val Lys Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly  
 195 200 205

Pro Asp Val Asp Ala Ala Asn Ala Asn Ala Asp Cys Val Met Leu Ala  
 210 215 220

Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys  
 225 230 235 240

Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly  
 245 250 255

Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val  
 260 265 270

Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr  
 275 280 285

Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu  
 290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala  
 305 310 315 320

Met Ala Ser Ala Leu Ala Asn Leu Val Glu Glu Ser Ser Arg Gln Leu  
 325 330 335

Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg  
 340 345 350

Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu  
 355 360 365

Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Thr Ala Gln Met Trp  
 370 375 380

Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala  
 385 390 395 400

Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala  
 405 410 415

Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn  
 420 425 430

Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr  
 435 440 445

Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe  
 450 455 460

Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly  
465 470 475 480

Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys  
485 490 495

Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser  
500 505 510

Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Pro Val Lys  
515 520 525